

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 04:47:34 ; Search time 116.57 Seconds

(Without alignments)  
534.256 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846  
Sequence: 1 MEPPKQGVDEFYDIGELG.....TEEDIAKKALHPRRSSNS 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_19:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhcc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rhodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriapi:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1835	99.4	370	4	075892	075892 homo sapien
2	1824	98.8	370	4	090UK4	090UK4 homo sapien
3	1764	95.6	370	11	090YM4	090YM4 mus musculu
4	1481	80.2	303	11	088861	088861 mus musculu
5	1297	70.3	1430	11	09JJP7	09JJP7 mus musculu
6	1293	70.0	367	4	09BRL8	09BRL8 homo sapien
7	1251.5	67.8	345	11	09CV44	09CV44 mus musculu
8	1166	63.2	454	4	043293	043293 mus musculu
9	1140	61.8	448	11	054784	054784 mus musculu
10	1140	61.8	448	11	088764	088764 ratu
11	787	42.6	1435	5	044997	044997 caenorhabd
12	698	37.8	992	4	09C0U5	09C0U5 homo sapien
13	695	37.6	641	6	09BES9	09BES9 macaca fasc
14	688.5	37.3	907	13	098850	098850 carassius a
15	668.5	36.2	611	11	091XS9	091XS9 cavia porce
16	665.5	36.1	2762	5	P91255	P91255 caenorhabd

17	660	35.8	1721	5	0961U1	0961U1 drosophila
18	660	35.8	7107	5	09VAE7	09VAE7 drosophila
19	651.5	35.3	371	11	091XS8	091XS8 ratu
20	650	35.2	6658	5	076281	076281 drosophila
21	649.5	35.2	372	11	0923E7	0923E7 mus musculu
22	641	34.7	795	4	096DV1	096DV1 homo sapien
23	621.5	33.7	451	5	016980	016980 aplysia cal
24	603.5	33.7	566	4	09H1R3	09H1R3 homo sapien
25	594	32.2	577	5	09GVE1	09GVE1 drosophila
26	592	32.1	929	5	001651	001651 drosophila
27	591	32.0	732	5	09GTV1	09GTV1 drosophila
28	591	32.0	786	5	09GV79	09GV79 drosophila
29	591	32.0	832	5	001653	001653 drosophila
30	591	32.0	913	5	09V7G6	09V7G6 drosophila
31	589	31.9	1211	5	023260	023260 caenorhabd
32	586	31.7	569	5	001652	001652 drosophila
33	584.5	31.7	6831	5	023550	023550 caenorhabd
34	584.5	31.7	7160	5	023551	023551 caenorhabd
35	581	31.5	1289	4	09Y2A5	09Y2A5 homo sapien
36	580	31.4	2959	11	09JTF1	09JTF1 ratu
37	578.5	31.3	446	5	0958K9	0958K9 drosophila
38	571.5	31.0	335	5	061269	061269 mytilus gal
39	571.5	31.0	878	5	09GV22	09GV22 mytilus gal
40	564	30.6	357	4	09HD31	09HD31 homo sapien
41	553.5	30.0	623	5	09GV80	09GV80 drosophila
42	547	29.6	343	4	09NNY2	09NNY2 homo sapien
43	545	29.5	343	11	070150	070150 ratu
44	544.5	29.5	343	11	09QYK9	09QYK9 mus musculu
45	544	29.5	342	11	008767	008767 ratu

# ALIGNMENTS

RESULT 1  
ID 075892 PRELIMINARY; PRT; 370 AA.  
AC 075892;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE DAP-KINASE RELATED PROTEIN 1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP  
RC TISSUE=KIDNEY;  
RX MEDLINE=20094983; PubMed=10629061;  
RA Indal B., Shant G., Cohen O., Kissil J.L., Kinchi A.;  
RT "Death-associated protein kinase-related protein 1, a novel  
Serine/Threonine kinase involved in apoptosis.";  
RL Mol. Cell. Biol. 20:1044-1054(2000).  
CC 1 - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AF052941; AAC35001.1; -  
DR HSP: Q63450; IAK6.  
DR InterPro: IPR00719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 370 AA; 42923 MW; 09502B4ADC020F91 CRC64;

Query Match 99.4%; Score 1835; DB 4; Length 370;  
Best Local Similarity 99.7%; Pred. No. 3.2e-125;  
Matches 359; Conservative 1; Indels 0; Gaps 0;  
QY 1 MEPPKQGVDEFYDIGELSGGFALVKKCKEKGSGLEVAKFKKRGSRASRGVSNE 60



QY	121	KOLDSVANTLHKRLAHFDLKPENIMLBDKNIP	1PHIKLIDFGLANHIEGVENKINFGT	180
Db	131	KOLDSVANTLHKRLAHFDLKPENIMLBDKNIP	1PHIKLIDFGLANHIEGVENKINFGT	190
QY	181	PEFVABEIVNEPPLGLEADMMISIVITVYILL	SGASPLDFTQKQETLANITSVSYDEDEEF	240
Db	191	PEFVABEIVNEPPLGLEADMMISIVITVYILL	SGASPLDFTQKQETLANITSVSYDEDEEF	250
QY	241	FSHTSELANDFIRKLIVETKRRKRLTIOEALR	NHWITPVNDQOAMRRRSVYNLENFRKQY	300
Db	251	FSQSTELANDFIRKLIVETKRRKRLTIOEALR	NHWITPVNDQOAMRRRSVYNLENFRKQY	310
QY	301	VRRRWKLFSFIVSLCNHLTRSLAMKVVHRLP	EDLRNCSPTDEEDLARKKALHPRRSSTS	360
Db	311	VRRRWKLFSFIVSLCNHLTRSLAMKVVHRLP	EDLRNCSPTDEEDLARKKALHPRRSSTS	370
RESULT	3			
Q9QYM4				
ID	Q9QYM4	PRELIMINARY:	PRT:	370 AA.
AC	Q9QYM4:			
DT	01-MAY-2000	(TREMblrel, 13, Created)		
DT	01-MAY-2000	(TREMblrel, 13, Last sequence update)		
DT	01-DEC-2001	(TREMblrel, 19, Last annotation update)		

OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Osteichthyes; Actinopterygii; Clupeiformes; Clupeidae; Muraenae; Muraena
NCBI_TaxID	10990;
RN	(1)
SEQUENCE FROM N.A.	
MEBLINE=99303018; PubMed=10376525;	
Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,	
Jenkins N.A., Akita S.;	
"Death-associated protein kinase 2 is a new calcium/calmodulin-	
dependent protein kinase that signals apoptosis through its catalytic	
activity.";	
Oncogene 18:3471-3480(1999)	
-1- SIMILARITY: BELONGS TO "THE SER/THR FAMILY OF PROTEIN KINASES.	
EMBL: AB018002; BAA8064.1; "	
HSSP: O63450; 1A06.	
MGI: MGI:1341297; Dapk2.	
InterPro: IPR000719; Euk_pkinase.	
InterPro: IPR002290; Ser_thr_kinase.	
InterPro: IPR001245; Tyr_pkinase.	
Pfam: PF00069; pkinase; 1.	
PRINTS: PR00109; TYRKINASE.	
SMART: SM00220; S_TKc_1.	
PROSITE: PS00107; PROTEIN_KINASE_APP; 1.	
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	
PROSITE: PS00108; PROTEIN_KINASE_ST_1.	
APP-binding; Kinase; Serine/threonine-protein kinase; Transferase.	
KW APP-binding; Kinase; Serine/threonine-protein kinase; Transferase.	
SQ	370 AA; 42769 MW; IDA629C4E661B3 CRC64;

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Db      11  HELIANGVNTLHNYITLHDVYENRFDVYHILELVSGSELDPLAOKESLSSEEAATSF 120
QY      61  TEREVSTLRQVLAHHNYITLHDVYENRFDVYHILELVSGSELDPLAOKESLSSEEAATSF 130
Db      71  TEREVSTLRQVLAHPNITLHDVYENRFDVYHILELVSGSELDPLAOKESLSSEEAATSF 140
QY      121  KQILDGVNNTLAHTKIAHPDLKPEMMLDKNIPPIPIKILDFGLAHEIDGVYEKNITGT 180
Db      131  KQILDGVNNTLAHTKIAHPDLKPEMMLDKNIPPIPIKILDFGLAHEIDGVYEKNITGT 190

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OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=TONGUE;
RC	MEDLINE=21085660; PubMed=11217851;
RA	Kawai Y., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanae I.,
RA	Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuenli P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J.,
RA	Schimi L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustringich S., Hall D., Hofmann L., Mashima J., Mazzarelli U., Mombaerts P.,
RA	Lyons P., Marchionni L., Mashima J., Hune D.A., Kamiya M., Lee N.H.,
RA	Nordone P., Rling B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Saito K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
RA	Hayashizaki Y.;
RT	Functional annotation of a full-length mouse cDNA collection.;
RL	Nature 409:685-690(2001).
DR	EMBL: AK009701; BMB26448.1; ..
DR	HSSP: Q63450; IAO6: 2310039H24R1K.
DR	MGD: MGI:1916885; 2310039H24R1K.
DR	InterPro: IPR000719; Euk-pkinase.
DR	InterPro: IPR002290; Ser_thr-kinase.
DR	InterPro: IPR001245; Tyr-kinase.
DR	Pfam: PF00069; pkinase; 1.
DR	PRINTS: PR00109; TYRKINASE.
DR	SMART: SM00220; S_TKC; 1.
DR	SMART: SM00219; TYTK; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
KW	ATP-binding; Transferase.
FT	NON_TER 345 345
SEQ	SEQUENCE 345 AA; 39776 MW; FF7D1B4F71CA93C0 CRC64;



AC	054784,	
DT	01-JUN-1998 (TRENDBIOL. 06, Created)	
DT	01-JUN-1998 (TRENDBIOL. 06, Last sequence update)	
DT	01-DEC-2001 (TRENDBIOL. 19, Last annotation update)	
DE	ZIP-KINASE.	
GN	DAPK3.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98147805; PubMed=9488481;	
RA	Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;	
RT	"Zip-kinase, a novel serine/threonine kinase which mediates	
RT	apoptosis";	
RL	Mol. Cell. Biol. 18:1642-1651(1998).	
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
DR	EMBL: AB007143; BAA24954.1; "-	
DR	HSSP: 063450; IAO6.	
DR	MGI: 1203520; DapK3.	
DR	InterPro: IPR000719; Ser_kinase.	
DR	InterPro: IPR002290; Ser_thr_kinase.	
DR	Pfam: PF00069; kinase.1.	
DR	SMART: SM00220; S_TKc. 1.	
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.	
DR	ATP-binding; Kinase; Serine/threonine protein kinase; Transferase	
QO	SEQUENCE 448 AA; 51421 MW; DA32F33B1F20EFC CRC64;	

[illegible]



OX NCBI\_TaxID=10116;  
 RN SEQUENCE FROM N.A.  
 RA Kogel D., Plotter O., Landsberg G., Christian S., Scheidtmann K.,  
 RT "Cloning and characterisation of Dlk, a novel serine/threonine kinase  
 RT that is tightly associated with chromatin and phosphorylates core  
 RT histones.";  
 RT Oncogene 20:2645-2654(1998).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AF006971; CA07360.1; .  
 DR HSSP: 063450; 1A06.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 448 AA; 51449 MW; 8430FDD0BF0C1EEA CRC64;

Query Match 61.8%; Score 1140; DB 11; Length 448;  
 Best Local Similarity 71.0%; Pred. No. 9, 7e-75;  
 Matches 225; Conservative 38; Mismatches 42; Indels 12; Gaps 2;

OY 1 MEPPKQKQVDFPDIGELSGGFALVKKCKREKSTGLEVAAKFIKKRQSRASRGVSRRE 60  
 1 MSTFRQDVEHHEMGELSGGFALVKKQCKGTGMEVAKFIKKRRRLPSSRRGVSREE 60  
 DB 1 IEREVSILROYLHNHNTLHDVYENKTDVYHIELVSGGELFPLAKOKESLSEETSPF 120  
 OY 61 IEREVSILROYLHNHNTLHDVYENKTDVYHIELVSGGELFPLAKOKESLSEETSPF 120  
 DB 61 IEREVSILREIRHNTLHDVYENKTDVYHIELVSGGELFPLAKOKESLSEETSPF 120  
 OY 121 KOIIDVNVYHTKRIAHFDKPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGT 180  
 DB 121 KOIIDVNVYHTKRIAHFDKPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGT 180  
 OY 121 KOIIDVNVYHTKRIAHFDKPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGT 180  
 DB 121 KOIIDVNVYHTKRIAHFDKPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGT 180  
 OY 181 PEFAPELVNTEPLGLEADMSIGVTYIILSGASPLGDTKQETLANITSVSDPDEEF 240  
 DB 181 PEFAPELVNTEPLGLEADMSIGVTYIILSGASPLGDTKQETLANITSVSDPDEEF 240  
 OY 240 PEFAPELVNTEPLGLEADMSIGVTYIILSGASPLGDTKQETLANITSVSDPDEEF 240  
 DB 240 PEFAPELVNTEPLGLEADMSIGVTYIILSGASPLGDTKQETLANITSVSDPDEEF 240  
 OY 241 FSHSEELKQDFRKLIVETKRLTIOGALRHHPITPVNQAMVRESVYVLENFRKQY 300  
 DB 241 FSHSEELKQDFRKLIVETKRLTIOGALRHHPITPVNQAMVRESVYVLENFRKQY 300  
 OY 241 FSHSEELKQDFRKLIVETKRLTIOGALRHHPITPVNQAMVRESVYVLENFRKQY 300  
 DB 241 FSHSEELKQDFRKLIVETKRLTIOGALRHHPITPVNQAMVRESVYVLENFRKQY 300  
 OY 301 VRRRWKLSFVSLCNH 317  
 DB 301 VRRRWKLSFVSLCNH 317  
 OY 289 RRRLRAARLREYSLKSH 305  
 DB 289 RRRLRAARLREYSLKSH 305

RESULT 11  
 OY 044997 PRELIMINARY; PRT: 1435 AA.  
 AC 044997;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE K12C11.4 PROTEIN.  
 GN K12C11.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Wamsley P., Kramer J.;  
 RT "The sequence of C. elegans cosmid K12C11.";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AF043701; AAK18971.1; .  
 DR HSSP: 063450; 1A06.  
 DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00023; ank; 7.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00248; ANK; 7.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS50088; ANK\_REPEAT; 7.  
 DR PROSITE: PS30297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ANK repeat; ATP-binding; Repeat; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1435 AA; 160602 MW; C73EB605C37FB732 CRC64;

Query Match 42.6%; Score 787; DB 5; Length 1435;  
 Best Local Similarity 47.9%; Pred. No. 1, 7e-48;  
 Matches 160; Conservative 63; Mismatches 105; Indels 6; Gaps 4;

OY 22 GGFALVKKCKREKSTGLEVAAKFIKKRQSRASRGVSRREIEREVSILROYLHNHNTLH 80  
 DB 80 GGFALVKKCKREKSTGLEVAAKFIKKRQSRASRGVSRREIEREVSILROYLHNHNTLH 80  
 OY 81 DVEYENKTDVYHIELVSGGELFPLAKOKESLSEETSPFIOIDGVNLYHTKRIAHFDL 140  
 DB 81 DVEYENKTDVYHIELVSGGELFPLAKOKESLSEETSPFIOIDGVNLYHTKRIAHFDL 140  
 OY 140 AVEYASDVYIYELVSGGELFPLAKOKESLSEETSPFIOIDGVNLYHTKRIAHFDL 199  
 DB 140 AVEYASDVYIYELVSGGELFPLAKOKESLSEETSPFIOIDGVNLYHTKRIAHFDL 199  
 OY 141 KPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGTPEFAPELVNTEPLGLEAD 200  
 DB 141 KPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGTPEFAPELVNTEPLGLEAD 200  
 OY 200 KPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGTPEFAPELVNTEPLGLEAD 257  
 DB 200 KPEINIMLDKNIPRIKIDFGIAHEIDEGVEKNIFGTPEFAPELVNTEPLGLEAD 257  
 OY 201 WSGIVTYIILSGASPLGDTKQETLANITSVSDPDEEFSTSELAKDFIRKLIVET 260  
 DB 201 WSGIVTYIILSGASPLGDTKQETLANITSVSDPDEEFSTSELAKDFIRKLIVET 260  
 OY 258 WAGVNVYIILSGASPLGDTKQETLANITSVSDPDEEFSTSELAKDFIRKLIVET 317  
 DB 258 WAGVNVYIILSGASPLGDTKQETLANITSVSDPDEEFSTSELAKDFIRKLIVET 317  
 OY 261 RKRLTIOGALRHHPITPVNQAMVRESVYVLENFRKQYVRRRWKLSFVSLCNH 320  
 DB 261 RKRLTIOGALRHHPITPVNQAMVRESVYVLENFRKQYVRRRWKLSFVSLCNH 320  
 OY 318 DQATVEECLOHPIRBPBGNAIDIRKASCITISHISFTRBQRMKCYELVAVYLKASK 377  
 DB 318 DQATVEECLOHPIRBPBGNAIDIRKASCITISHISFTRBQRMKCYELVAVYLKASK 377  
 OY 321 SLARKVHLRPDED--LRNCSDTEEDTARKKALH 352  
 DB 321 SLARKVHLRPDED--LRNCSDTEEDTARKKALH 352  
 OY 378 SSRIGCGRFEDEDMVASCTLCAEE--GNLRALH 410  
 DB 378 SSRIGCGRFEDEDMVASCTLCAEE--GNLRALH 410

RESULT 12  
 OY 09C0L5 PRELIMINARY; PRT: 992 AA.  
 AC 09C0L5;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE MYOSIN LIGHT CHAIN KINASE.  
 GN MLCK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL LOBE LEFT;
RA Oosada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain CDNA
RT libraries."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL AB056801; BAB93325.1; -.
DR HSSP; P56276; 1TKL.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

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SEQUENCE	641 AA: 72195 MW: 48BA0621851868E CRC64:
Query Match	37.6%; Score 695; DB 6; Length 641;
Best Local Similarity	41.6%; Pred. No. 2.8e-42;
Matches 146: Conservative	65: Mismatches 118; Indels 22; Gaps
0Y	6 QOKVDEFDIGELSSGCGFATYKCKREKSTGLEYAKFPKKQSRASRGVSRRELEERY 65
Db	257 EQKVVDDVDIERLSSGKGGVFRVLEKTRKIMAGKFKAYSAR-----EKENRROI 310
0Y	66 SILRQVLHNVTYTLHDVYENFRDVHILIELVSGGELFDLQAE-SLSEEAFTSFQTL 124
Db	311 SIMNCLNHPKLVQCVDAPEEKANIYVLEIVSGGELFPEALIDEDPELTRECIKYMROS 370
0Y	125 DGVNVLHTKKIANHFDLKPENIMLQDNIPRIPIKLIDFGLAHEIEDGVGEFKINIGTPFV 184
Db	371 EGVEYIHKOGIYHMLDLKPEIMCVNKT--GTBIKIKLIDELARLLEDAGSLKVLFGTPFV 428
0Y	185 APEIYNVPELIGLEADWMSIGVTYLLISGASPLDGTQETLANITSVSDDEEFSHT 244
Db	429 APEVINTEPIGATIDWMSIGVCIYLLVSGLSEFPKGDNDNETANITSATWDDDEAFDEI 488
0Y	245 SELAFDITRLKLVETKTRKRLTIOEALRHPI-TPYDNOQAMVRRSVNLENFRRQYVR 303
Db	489 SDDADFISNLLKDKMKRNLDCTQCLQHPMLKDKRKNMBA-----KLSDKBKKYMMAR 543
0Y	304 RKKLEFSIYSLCNHLTRSLM-----KKVHLRPDEDLRNCSDTDPEEDKL 347
Db	544 KWQKGNVRAIGRLSSMAMISGLSGKRSSTGSPISPLAERKLESEEDVSQ 594
RESULT 14	
ID 098850	PRELIMINARY: PRT: 907 AA.
AC 098850.	
DT 01-FEB-1997 (TREMBLrel. 02, Created)	
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)	



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DT      01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE      MYOSIN LIGHT CHAIN KINASE (FRAGMENT).
GN      MYCK.
OS      Cavia porcellus (Guinea pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystriognathli; Cavidae; Cavia.
OX      NCBI_TaxID=10141;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BASAL ARTERY;
RA      Nakamura A., Liu L., Hanyuda Y., Kohama K.;
RT      "Molecular cloning of myosin light chain kinase of the cells derived
RL      from Guinea pig vascular smooth muscle.";
DR      Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
KW      KINase.
FT      1
FT      NON-TER      1
SQ      SEQUENCE      611 AA; 68810 MW; 14B6F874B6E6A7F5 CRC64;

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Query Match	36.2%	Score 668.5	DB 11	Length 611
Best local similarity	44.2%	Pred. No. 2.2e-40		
Matches 134	Conservative 56	Mismatches 98	Indels 15	Gaps 5
QY	6	QAKVEDFYDIGELSGGCGFAIVKCKREKSTGLEVAKEPIKKRQSRASRGVSGREIREV	65	
Db	316	EOKVSYLDYDEELSGSGKFGQVFLVERKLEKIMVKGFFKVAYSK-----EKNIMEI	369	
QY	66	SILROYLHNVAIVLHNVYENRTDVIHLELVSGGLFDFLQAK-SISEEATSFIKOIL	124	
Db	370	GIMMCLHNRKYQVDAFEKANIVAVLEIVSGGLFEFIIDDELTERECIQYMQIS	429	
QY	125	DGVNVLTKKIAHPDLKPRNIMLDKNIFPIPIKILIDFLAHEIDGVYEFKNIGSTPEV	184	
Db	430	EGVEYIKRQGIVHDLKPRNIMCVNKT--GTRKILIDFLARLRLNAGSLKLVETPEFV	487	
QY	185	APELYNEEPLGLEADWMSIGVITYLLSGASPLSGTQKETAITSVYSDDEEFFSHT	244	
Db	488	APELYNEEPLGYATIDWMSIGVICYIIVSGISPPMGNDDELTANVYSATWDDDEDAFBI	547	
QY	245	SELAKDFIRKLVLKETKRLTIOEALRHPI--PPVYNQOAMVRESVVLNENFKQYAR	303	







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